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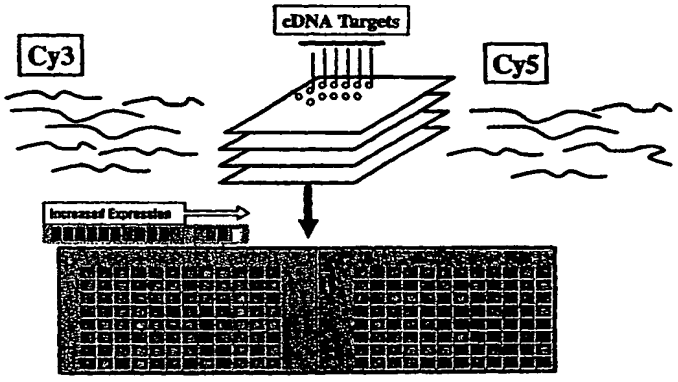
(81) Designated States *(national)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States *(regional)*: ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SI, SK,

[Continued on next page]

(54) Title: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY OF HEMATOLOGICAL MALIGNANCIES

Outline of Microarray Chip Technology approach



(57) Abstract: Disclosed are methods and compositions for the detection, diagnosis, prognosis, and therapy of hematological malignancies, and in particular, B cell leukemias, lymphomas and multiple myelomas. Disclosed are compositions, methods and kits for eliciting immune and T cell responses to specific malignancy-related antigenic polypeptides and antigenic polypeptide fragments thereof in an animal. Also disclosed are compositions and methods for use in the identification of cells and biological samples containing one or more hematological malignancy-related compositions, and methods for the detection and diagnosis of such diseases and affected cell types. Also disclosed are diagnostic and therapeutic kits, as well as methods for the diagnosis, therapy and/or prevention of a variety of leukemias and lymphomas.

WO 03/062401 A2

TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Declarations under Rule 4.17:

— *as to applicant's entitlement to apply for and be granted a patent (Rule 4.17(ii)) for the following designations AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VC, VN, YU, ZA, ZM, ZW, ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG)*

— *as to the applicant's entitlement to claim the priority of the earlier application (Rule 4.17(iii)) for all designations*

— *of inventorship (Rule 4.17(iv)) for US only*

Published:

— *without international search report and to be republished upon receipt of that report*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

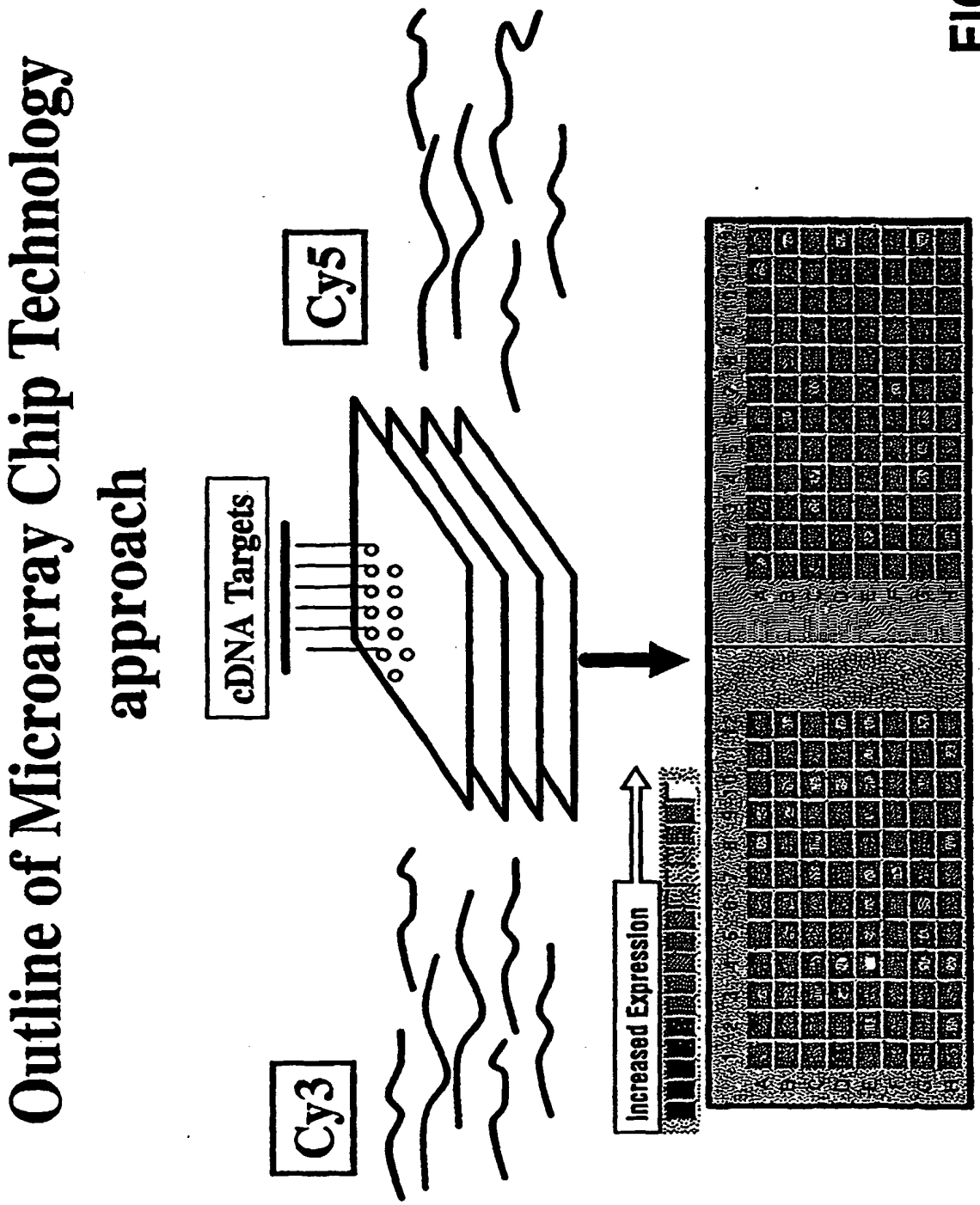

Outline of Microarray Chip Technology approach
cDNA Targets
Cy5
Cy3
Increased Expression

FIG. 1

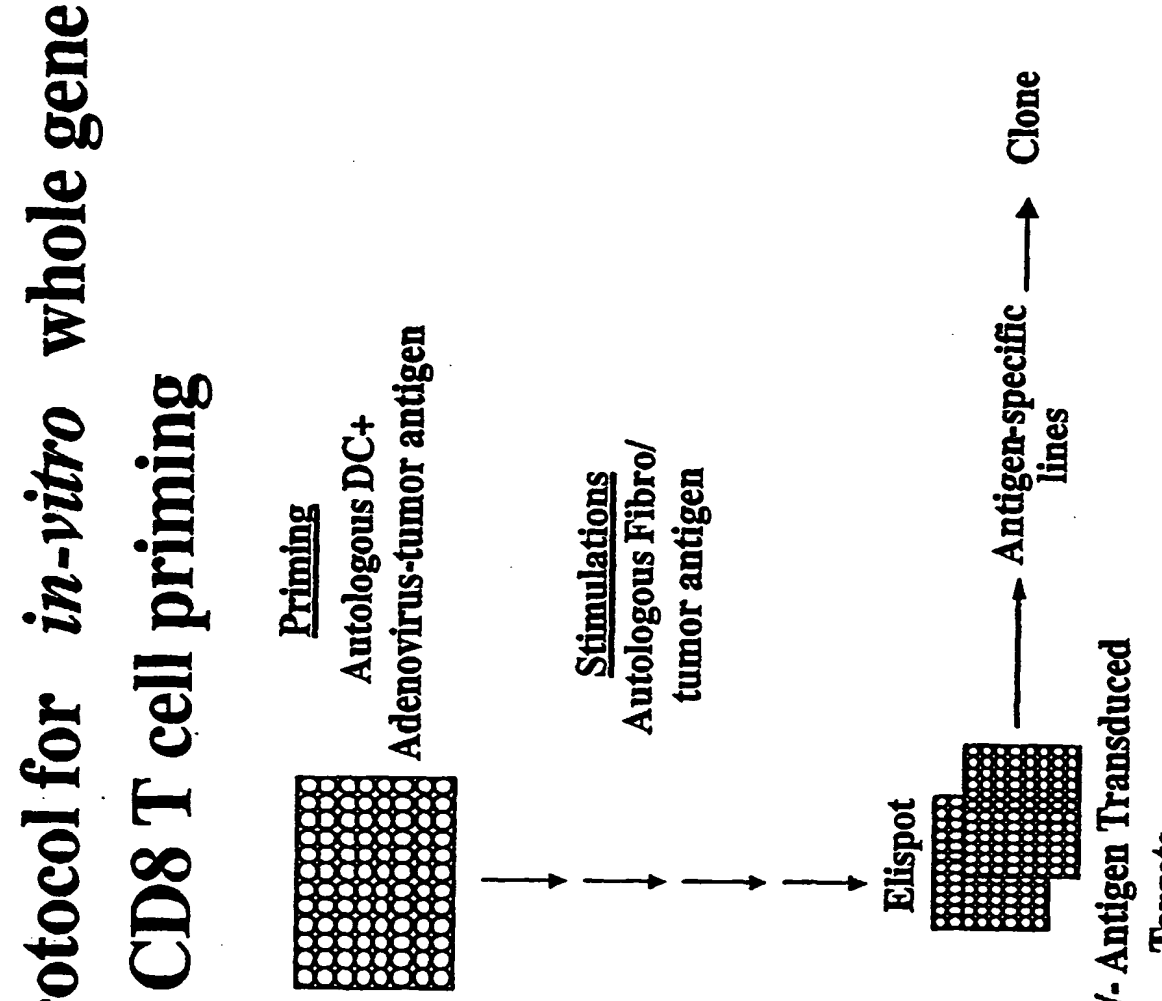

General protocol for *in-vitro* whole gene CD8 T cell priming
Priming
Autologous DC+ Adenovirus-tumor antigen
Stimulations
Autologous Fibro/ tumor antigen
Elispot
+/- Antigen Transduced Targets
Antigen-specific lines
Clone

FIG. 2

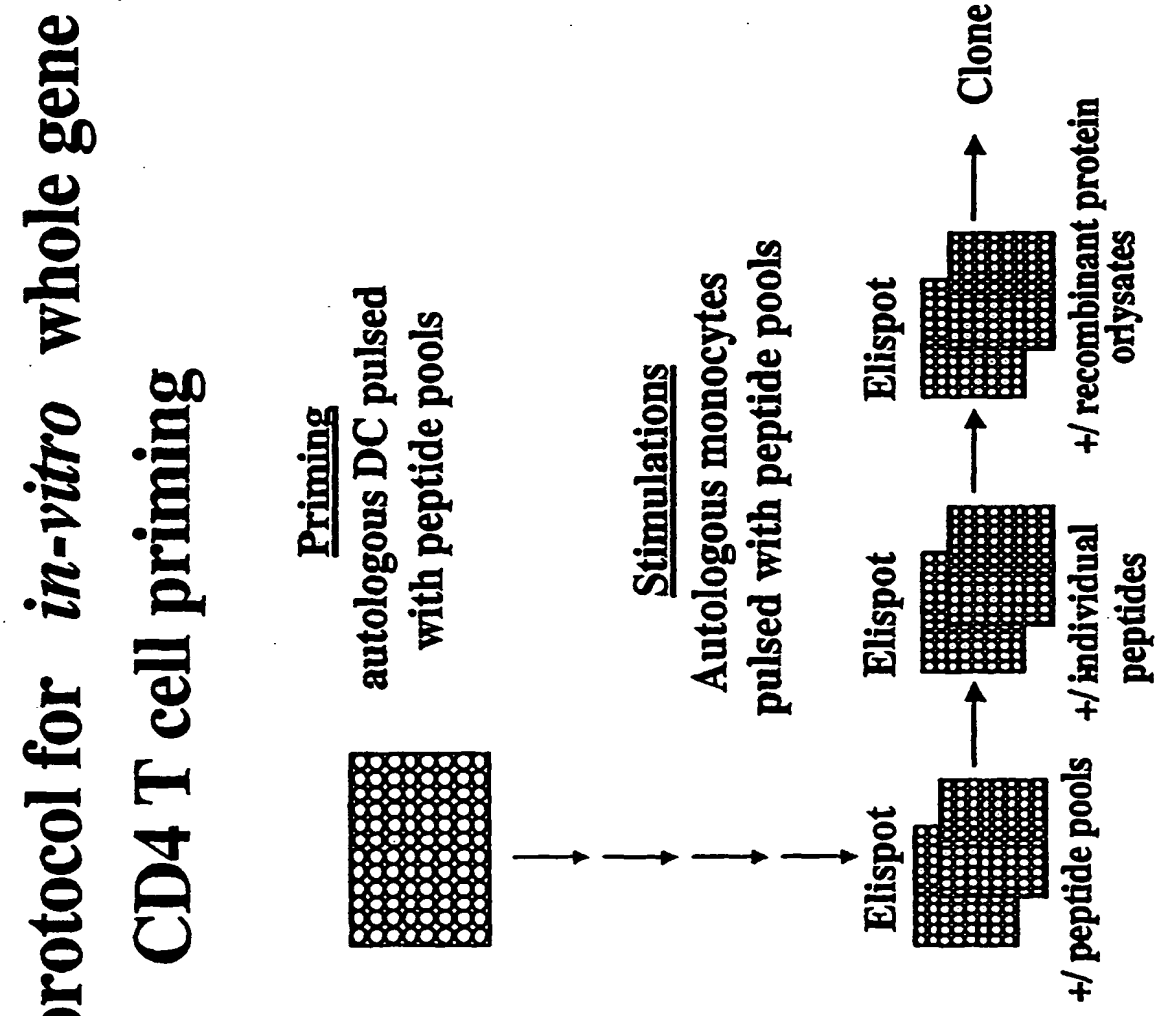

General protocol for *in-vitro* whole gene
CD4 T cell priming
Priming
autologous DC pulsed
with peptide pools
Stimulations
Autologous monocytes
pulsed with peptide pools
Elispot
+/ peptide pools
Elispot
+/ individual
peptides
Elispot
+/ recombinant protein
orlysates
Clone

FIG. 3

LEUKEMIA/LYMPHOMA CHIP #3: PROBES USED IN ANALYSIS

Cy3 Probe		Cy5 Probe	
Tissue	RNA#	RNA#	Tissue
Lymphoma, T cell	952	SPACT74	Kidney N
Lymphoma, B cell	955	SPACT81	Liver N
Lymphoma, B cell	953	SPACT78	Lung N
Lymphoma	916	SPACT42	Brain N
Lymphoma, Hodgkins	950	138598B	Skin N
Lymphoma, Hodgkins	950	SPACT49	Bone Marrow N
Lymphoma, B cell	CL151	888	PBMC resting
Lymphoma, T cell	904B	SPACT55	Stomach N
Lymphoma, Hodgkins see RNA 959	CL153	SPACT70	Thymus N
Lymhoma, B cell	CL152	SPACT75	Skeletal Muscle N
Lymphoma, B cell see RNA 958	CL155	SPACT73	Heart N
Lymphoma, B cell	944	243502B	Esophagus N
Lymphoma, B cell	958	1006	Colon N
Lymphoma, B cell	954	SPACT65	Small Intestine N
Lymphoma	960	779B	Trachea N
Lymphoma, T cell	957	S9327328	Bladder N
Lymphoma, B cell	914B		
Lymphoma, B cell	913		
Lymphoma, B cell	944B		
Lymphoma, B cell/failed	903		

GREEN: Tumor probes where gene expression would be desired.
RED: Normal essential tissue probes where gene expression is to be avoided.
BLACK: Normal tissue probes where gene expression is acceptable.

FIG. 4

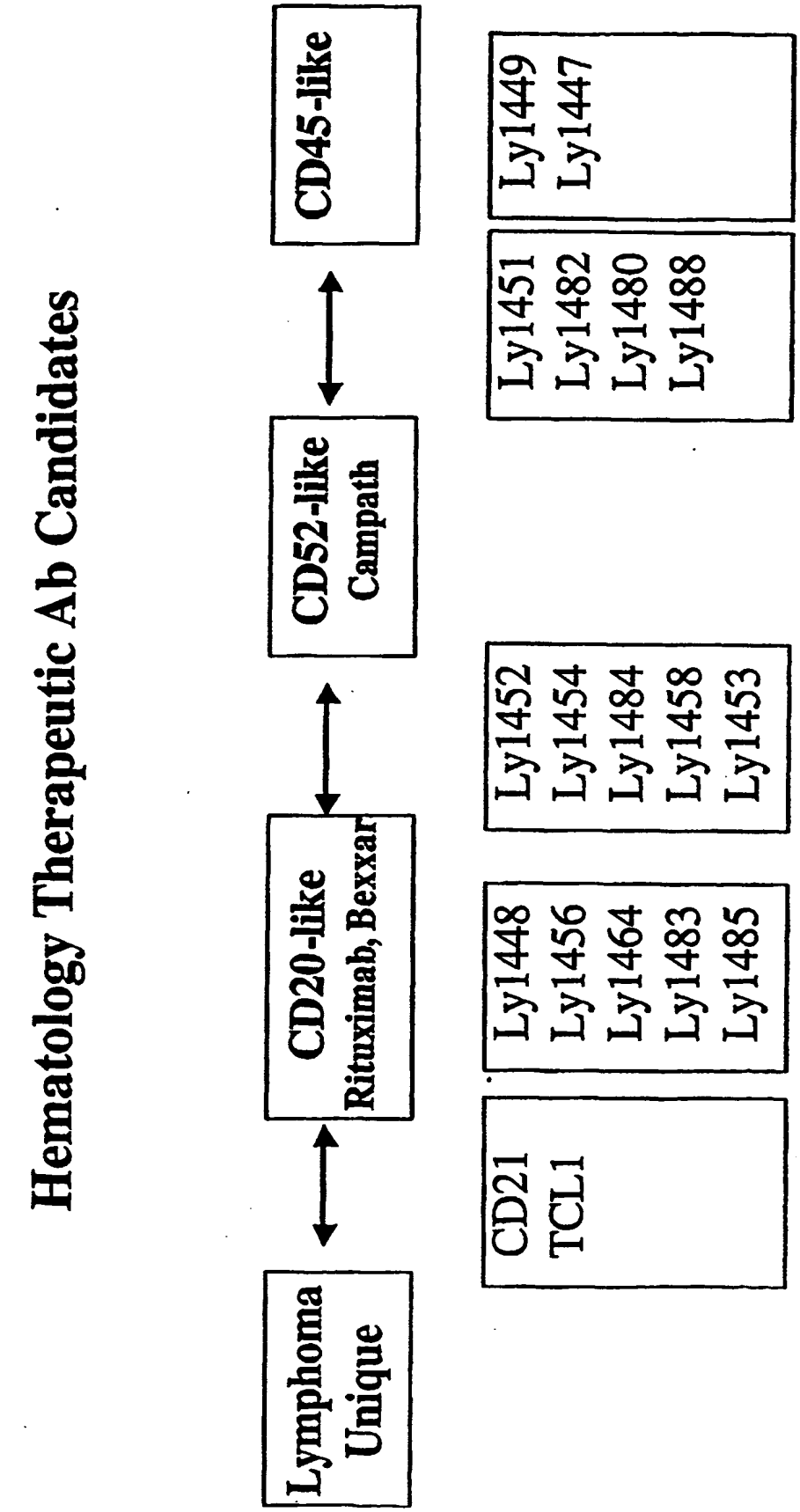

Hematology Therapeutic Ab Candidates
Lymphoma Unique
CD20-like Rituximab, Bexxar
CD52-like Campath
CD45-like
CD21
TCL1
Ly1448
Ly1456
Ly1464
Ly1483
Ly1485
Ly1452
Ly1454
Ly1484
Ly1458
Ly1453
Ly1451
Ly1482
Ly1480
Ly1488
Ly1449
Ly1447

FIG. 5

a. TMpred Report for Ly1484 Long

Date: 8/15/2001

RDFQSEVLLSAMELFHMTSGGDAAMFRDGKEPQPSAEAAAAPSLANISCF
TQKLVEKLYSGMFSADPRHLLLFILEHIMVVIETASSQRDTVLSTLYSSL
NKVILYCLSKPQQSLSECLGLLSILGFLQEHWDVVFATYNSNISFLLCLM
HCLLLLNERSYPEGFGLEPKPRMSTYHQVFLSPNEDVKEKREDLPSLSDV
QHNIQKTVQTLWQQLVAQRQQTLEDAFKIDLSVKPGEREVKIEEVTPLWE
ETMLKAWQHYLASEKKSLASRSNVAHHSKVTLWSGSLSSAMKLMPGRQAK
DPECKTEDFVSCIENYRRRGQELYASLYKDHVQRRKCGNIKAANAWARIQ
EQLFGELGLWSQGEETKPCSPWELDWREGPARMRKRIKRLSPLEALSSGR
HKESQDKNDHISQTNAENQDELTLREAEGEPDEVGVDCTQLTFFPALHES
LHSEDFLELCRERQVILQELLDKEKVTQKFSLVIVQGHLVSEGVLLFGHQ
HFYICENFTLSPTGDVYCTRHCLSNISDPFIFNLCSKDRSTDHYSCQCHS
YADMRELRQARFLLQDIALEIFFINGYSKFLVFYNNDRSKAFKSFCSFQP
SLKGKATSEDTLNLRRYPGSDRIMLQKWQKRDISNFEYLMYLNTAAGRTC
NDYMQYPVFPWVLADYTSETLNLANPKIFRDLSKPMGAQTKERKLKFIQR
FKEVEKTEGDMTVQCHYYTHYSSAIIVASYLVRMPPFTQAFCALQGGSFD
VADRMFHSVKSTWESASRENMSDVRELTPEFFYLPEFLTNCNGVEFGCMQ
DGTVLGDVQLPPWADGDPRKFISLHRKALESDFVSANLHHWIDLIFGYKQ
QGPAAVDAVNLFHPYFYGDRMDLSSITDPLIKSTILGFVSNFGQVPKQLF
TKPHPARTAACKPLPGKDVSTPVSLPGHPQPFFYSLQSLRPSQVTVKDMY
LFSLGSESPKGAIGHIVSTEKTILAVERNKVLLPPLWNRTFSWGFDDFSC
CLGSYGSDKVLMTFENLAAWGRCLGAVGPSPTTIVTSGTSTVVCVWELSM
TKGRPRGLRLRQALYGHTQAVTCLAASVTFSLLVSGSQDCTCLLWDLDHL
THVTRLPAHREGISATTISDVSGTIVSCAGAHLSLWNVNGQPLASITTAW
GPEGATCCGLMEGPAWDTSQILLTGSQDGMVRVWKTEDVKMSVPGRPAG
EEPLAQPPSPRGHKWEKNLALSRELDVSTALTGKPSKTSPAVTALAVSRN
HTKLLVGDERGRTFCWSADG (SEQ ID NO: 10,847)

Black = Intracellular, Red = Transmembrane,
Blue = Extracellular

Ly1484 Long has 1269 amino acids and 5
Transmembrane Domains

Transmembrane Domain 1:	63 - 84	Score: 1.36675
Transmembrane Domain 2:	118 - 139	Score: 1.38695
Transmembrane Domain 3:	480 - 501	Score: 1.36185
Transmembrane Domain 4:	562 - 583	Score: 1.31785
Transmembrane Domain 5:	725 - 746	Score: 1.3521

FIG. 6

b. TMpred Report for Ly1484 (short)

Date: 8/20/2001

MLQKWQKRDISNFEYLMYLNTAAGRTCNDYMQYPVFPWVLADYTSETLNL
ANPKIFRDLSKPMGAQTKERKLKFIQRFKEVEKTEGDMTVQCHYYTHYSS
AIIVASYLVRMPPFTQAFCALQGGSFDVADRMFHSVKSTWESASRENMSD
VRELTPEFFYLPEFLTNCNGVEFGCMQDGTVLGDVQLPPWADGDPRKFLS
LHRKALESDFVSANLHHWIDLIFGYKQQGPAAVDAVNIFHPYFYGDRMDL
SSITDPLIKSTILGFVSNFGQVPKQLFTKPHPARTAAGKPLPGKDVSTPV
SLPGHPQPFFYSLQSLRPSQVTVKDMYLFSLGSESPKGAIGHTVSTEKTI
LAVERNKVLLPPLWNRTFSWGEDDFSCCLGSYGSDKVLMTFENLAAWGRC
LCAVCPSPTTIVTSGTSTVVCVWELSMTKGRPRGLRLRQALYGHTQAVTC
LAASVTFSLLVSGSQDCTCILWDLDHLTHVTRLPAHREGLSAITTSDVSG
TIVSCAGAHLSLWNVNGQPLASITTAWGPEGAITCCCLMEGPAWDTSQLI
ITGSQDGMVRVWKTEDVKMSVPGRPAGEEPLAQPPSPRGHKWEKNLALSR
ELDVSTALTGKPSKTSPAVTALAVSRNHTKLLVGDERGRLFCWSADG

(SEQ ID NO: 10,848)

Black = intracellular, Red = Transmembrane,
Blue = Extracellular

Ly1484 has 646 amino acids and 1 Transmembrane Domains

Transmembrane Domain 1: 102 - 123 Score: 1.3521

FIG. 6 (cont.)

```
ANALYSIS RESULTS OF THE PROGRAM TSITES.

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AMPHI Window size: 11

A-AMPHI mid points of blocks.
R-Residues matching the Rothbard/Taylor motif.
D-Residues matching the IAd motif.
d-Residues matching the IEd motif.
```

(SEQ ID NO: 10,847)

```
     5    10    15    20    25    30    35    40    45    50    55    60    65    70    75
RDFQSEVLLSAMELFHMTSGGDAAMFRDGKEPQPSAEAAAAPSLANISCFTQKLVEKLYSGMFSADPRHILLFIL
..........AAAAA.....................AAAA.AAA....AAAAAAAAAAA.............
.....RRRRR..RRRRRRR.....................................RRRRRRRRRRRR.........
.....................................DDDDDD.................................
.....................................................................................

   80   85   90   95   100  105  110  115  120  125  130  135   140   145   150
EHIMVVIETASSQRDTVLSTLYSSLNKVILYCLSKPQQSLSECLGLLSILGFLQEHWDVVFATYNSNISFLLCLM
..................AAAAAAAA.........AAAAAAAAAAAAAAAAAAAAAAA.................
.......RRRR...RRRRR.........................RRRR..RRRR.....................
......DDDDDD.....DDDDDDD.............................................................
.....................................................................................
```

FIG. 7

```
  155  160  165  170  175  180  185  190  195  200  205  210  215  220  225
HCLLLLNERSYPEGFGLEPKPRMSTYHQVFLSPNEDVKEKREDLPSLSDVQHNIQKTVQTLWQQLVAQRQQTLED
.....................................AAAAA.AAAAAAAAAAAAA.....
.....................................RRRR.............R
.....
.....

  230  235  240  245  250  255  260  265  270  275  280  285  290  295  300
AFKIDLSVKPGEREVKIEEVTPLWEETMLKAWQHYLASEKKSLASRSNVAHHSKVTLWSGSLSSAMKLMPGRQAK
...................AAAA...AAAAAAAA.....................AAAAAAAA.....
RRR.....................RRRRRRRRRRRRR.....................RRRRR....
.....
.....dddd.....

  305  310  315  320  325  330  335  340  345  350  355  360  365  370  375
DPECKTEDFVSCIENYRRRGQELYASLYKDHVQRRKCGNIKAANAWARIQEQLFGELGLWSQGEETKPCSPWELD
......AAAAAAA.........AAAAAA.........AAAAAAAAAAAAAAA.............AAA.....
.......RRRR.........RRRRR.............RRRR.............RRRR.............
.....
.....

  380  385  390  395  400  405  410  415  420  425  430  435  440  445  450
WREGPARMRKRIKRLSPLEALSSGRHKESQDKNDHISQTNAENQDELTLREAEGEPDEVGVDCTQLTFFPALHES
....AAAAAAAAAAAAAAAAA.....................................AAAA.AAAA.
.................RRRR.....................RRRRR.....................
.................DDDDDD.....................DDDDDD.....................
.........dddd.....
```

FIG. 7 (cont.)

```
  455  460  465  470  475  480  485  490  495  500  505  510  515  520  525
LHSEDFLELCRERQVILQELLDKEKVTQKFSLVIVQGHLVSEGVLLFGHQHFYICENFTLSPTGDVYCTRHCLSN
...AAAAA.....................................................................AAAA
....RRRR.........RRRR..RRRR.........RRRR.....................................
.............................................................................
.............................................................................

  530  535  540  545  550  555  560  565  570  575  580  585  590  595  600
ISDPFIFNLCSKDRSTDHYSCQCHSYADMRELRQARFLLQDIALEIFFHNGYSKFLVFYNNDRSKAFKSFCSFQP
A.AAAAAA..............AAAAAAAAAAA.................................AAAAAA...
.....................................RRRRRRRRRRRRR..............RRRR.......
.............................................................................
.............................................................................

  605  610  615  620  625  630  635  640  645  650  655  660  665  670  675
SLKGKATSEDTLNLRRYPGSDRIMLQKWQKRDISNFEYLMYLNTAAGRTCNDYMQYPVFPWVLADYTSETLNLAN
.............AAAAA.........AAA............AAAAAAAAAA.......................
....RRRR.RRRR........RRRRR.............................RRRR.........RRRRRRRR...
.DDDDDD......................................................................
.............................................................................

  680  685  690  695  700  705  710  715  720  725  730  735  740  745  750
PKIFRDLSKPMGAQTKERKLKFIQRFKEVEKTEGDMTVQCHYYTHYSSAIIVASYLVRMPPFTQAFCALQGGSFD
AAAAAAAAAAAA........AAAAAAAAAAAA.........AAAAA.............................A
.RRRR...............RRRR..........RRRRR.RRRRR.............................R
```

FIG. 7 (cont.)

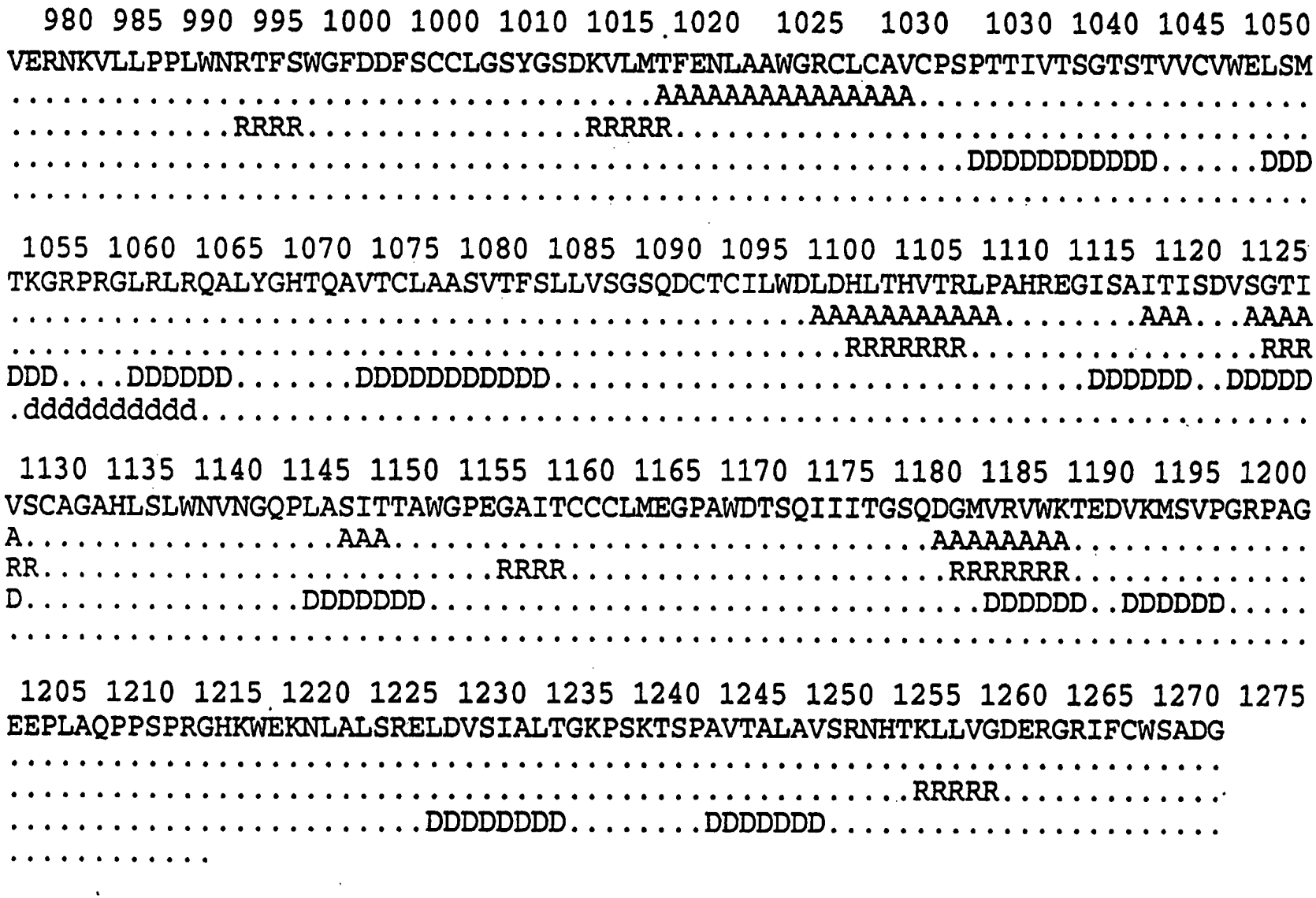
```
.....DDDDDDDDDD.....
.....dddd.....
.....

  755  760  765  770  775  780  785  790  795  800  805  810  815  820  825
VADRMFHSVKSTWESASRENMSDVRELTPEFFYLPEFLTNCNGVEFGCMQDGTVLGDVQLPPWADGDPRKFISLH
AAAAAAAAAA.AA.AAAA..AAAAAA.....AAAAAA.....AAA.....
RRRRRRR.....RRRRR.....RRRRR.....RRRRR.....RRRR..
.....
.....
.....

  830  835  840  845  850  855  860  865  870  875  880  885  890  895  900
RKALESDFVSANLHHWIDLIFGYKQQGPAAVDAVNIFHPYFYGDRMDLSSITDPLIKSTILGFVSNFGQVPKQLF
.....AAAAAAAAAA.....AAAAAAAAAAAA.....AAAAA..AAAAAAAAAAAAAAAA
.RRRR.RRRR....RRRRRRRR.....RRRR.....RRRR.....
.....DDDDDD.....
.....
.....

  905  910  915  920  925  930  935  940  945  950  955  960  965  970  975
TKPHPARTAAGKPLPGKDVSTPVSLPGHPQFFYSLQSLRPSQVTVKDMYLFSLGSESPKGAIGHIVSTEKTILA
.....AAAAAAAAA.....AAAAAAA.....
.....RRRRR.....RRRRRRRR.....
.....DDDDDD.....DDDDDD...
.....
.....
```

FIG. 7 (cont.)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VERNKVLLPPLWNRTFSWGFDDFSCCLGSYGSDKVLMTFENLAAWGRCLCAVCPSPTTIVTSGTSTVVCVWELSM
AAAAAAAAAAAAAAA
RRRR
RRRRR
DDDDDDDDDDD
DDD
1055 1060 1065 1070 1075 1080 1085 1090 1095 1100 1105 1110 1115 1120 1125
TKGRPRGLRLRQALYGHTQAVTCLAASVTFSLLVSGSQDCTCILWDLDHLTHVTRLPAHREGISAITISDVSGTI
AAAAAAAAAAA
AAA
AAAA
RRRRRRR
RRR
DDD
DDDDDD
DDDDDDDDDDD
DDDDDD
DDDDD
ddddddddddd
1130 1135 1140 1145 1150 1155 1160 1165 1170 1175 1180 1185 1190 1195 1200
VSCAGAHLSLWNVNGQPLASITTAWGPEGAITCCCLMEGPAWDTSQIIITGSQDGMVRVWKTEDVKMSVPGRPAG
A
AAA
AAAAAAAA
RR
RRRR
RRRRRRR
D
DDDDDDD
DDDDDD
DDDDDD
1205 1210 1215 1220 1225 1230 1235 1240 1245 1250 1255 1260 1265 1270 1275
EEPLAQPPSPRGHKWEKNLALSRELDVSIALTGKPSKTSPAVTALAVSRNHTKLLVGDERGRIFCWSADG
RRRRR
DDDDDDDD
DDDDDDD

FIG. 7 (cont.)

FIG. 8

ANALYSIS RESULTS OF THE PROGRAM TSITES.

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Mon, Aug 27,2001 10:34:51 AM
These are the results of the analysis of the file--> LY1484~2.TXT
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AMPHI Window size: 11

A-AMPHI mid points of blocks.
R-Residues matching the Rothbard/Taylor motif.
D-Residues matching the IAd motif.
d-Residues matching the IEd motif.

:Q ID NO:
10,848)

```
          5    10    15    20    25    30    35    40    45    50    55    60    65    70    75
MLQKWQKRDISNFEYLMYLNTAAGRTCNDYMQYPVFPWVLADYTSETLNLANPKIFRDLSKPMGAQTKERKLKFI
.....AAA.............AAAAAAAAAA.....................AAAAAAAAAAAA........AAA
.........................RRRR.........RRRRRRRR....RRRR..................RRR
.....................................................................................
.....................................................................dddd..

          80   85   90   95   100  105  110  115  120  125  130   135   140   145   150
QRFKEVEKTEGDMTVQCHYYTHYSSAIIVASYLVRMPPFTQAFCALQGGSFDVADRMFHSVKSTWESASRENMSD
AAAAAAAAA.........AAAAA.............................AAAAAAAAAAAA.AA.AAAA..AA
R..........RRRRR.RRRRR.............................RRRRRRRR.................
.....................DDDDDDDDDDD.....................................................
.....................................................................................

          155  160  165  170  175  180  185  190  195  200  205  210  215  220  225
VRELTPEFFYLPEFLTNCNGVEFGCMQDGTVLGDVQLPPWADGDPRKFISLHRKALESDFVSANLHHWIDLIFGY
AAAA.........AAAAAA................AAA.............................AAAAAAAAA...
..RRRRR.....RRRRR.............RRRRR.............RRRR...RRRR.RRRR....RRRRRRRR.
.....................................................................................
.....................................................................................
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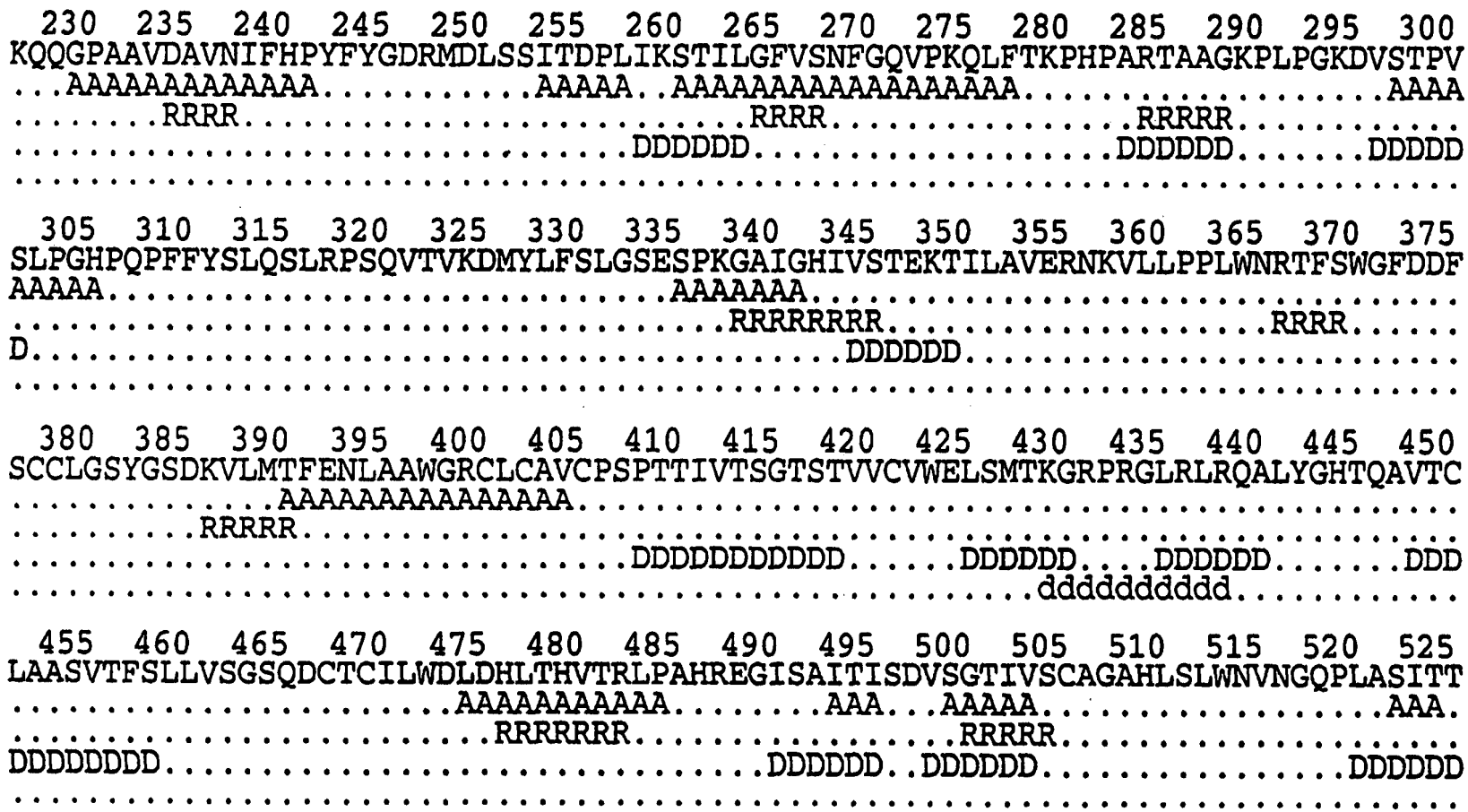

FIG. 8 (cont.)

```
  530   535   540   545   550   555   560   565   570   575   580   585   590   595   600
AWGPEGAITCCCLMEGPAWDTSQIIITGSQDGMVRVWKTEDVKMSVPGRPAGEEPLAQPPSPRGHKWEKNLALSR
.....AAAAAAA..........................................................
.....RRRR.....RRRRRRR..................................................
D.....DDDDDD..DDDDDD..................................................
.....................................................................
.....................................................................

  605   610   615   620   625   630   635   640   645   650   655   660   665   670   675
ELDVSIALTGKPSKTSPAVTALAVSRNHTKLLVGDERGRIFCWSADG
.....................RRRRR.....................
.....................RRRRR.....................
.DDDDDDD.....DDDDDD..ddddd.....................
.....................ddddd.....................
```

FIG. 8 (cont.)

INFORMAL SEQUENCE LISTING

<210> 1
<212> DNA
<213> Homo sapiens

<400> 1
1>Ly1728P, membrane protein FOAP-12, full-length cDNA
cttccagagagcaatatggctggttccccaacatgcctcaccctcatctatatccttggcagctcacag
ggtcagcagcctctggacccgtgaaagagctggtcggttccgttggtggggccgtgactttccccctgaa
gtccaaagtaaagcaagttgactctattgtctggaccttcaacacaacccctcttgtcaccatacagcca
gaaggggcactatcatagtgacccaaaatcgtaatagggagagagtagacttcccagatggaggctact
ccctgaagctcagcaaactgaagaagaatgactcagggatctactatgtggggatatacagctcatcact
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<210> 2
<212> PRT
<213> Homo sapiens

<400> 2

2>Ly1728P, FOAP-12, full-length protein
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IVTQNRNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHVYEHLSKPKVTMGLQSN
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<210> 3
<212> DNA
<213> Homo sapiens

<400> 3

3>Ly1732P, BCM, full-length cDNA

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<210> 4
<212> PRT
<213> Homo sapiens

<400> 4

4>Ly1732P, BCM, full-length protein
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<210> 5
<212> DNA
<213> Homo sapiens

<400> 5

5>Ly1888P, anti-Fas-induced apoptosis (TOSO), full-length cDNA
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<210> 6
<212> PRT
<213> Homo sapiens

<400> 6

6>Ly1888P, anti-Fas-induced apoptosis (TOSO), full-length protein
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EYKGRVTLKQYPRKNLFLVEVTQLTESDSGVYACGAGMNTDRGKTQKVTLNVHSEYEPSWEEQPMPETPK
WFHLPYLFQMPAYASSSKFVTRVTTPAQRGKVPPVHHSSPTTQITHRPRVSRASSVAGDKPRTFLPSTTA
SKISALEGLLKPQTPSYNHHTRLHRQRALDYGSQSGREGQGFHILIPTILGLFLLALLGLVVKRAVERRK
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<210> 7
<212> DNA
<213> Homo sapiens

<400> 7

7>Ly1452_His-tag-fusion, Old-SEQ-ID_10482, full-length cDNA
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<210> 8
<212> PRT
<213> Homo sapiens

<400> 8

8>Ly1452_His-tag-fusion, Old-SEQ-ID_10483, full-length protein
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SASPHGSSEKSSSFSLSSTEVHMVRPGYSHRVSLPTSPGILATSPYPETDSAFFEPSHLT
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LESVASAAT

<210> 9
<212> DNA
<213> Homo sapiens

<400> 9

9>Ly1452P_LS_400351.4_Edited, splice-1, full-length cDNA
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<210> 10
<212> PRT
<213> Homo sapiens

<400> 10

10>Ly1452P_LS_400351.4_Edited, splice-1, full-length protein
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<210> 11

<212> DNA
<213> Homo sapiens

<400> 11

11>Ly1452P, splice-2, FLJ21562, full-length cDNA
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<210> 12
<212> PRT
<213> Homo sapiens

<400> 12

12>Ly1452P, splice-form-2, FLJ21562, full-length protein
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QVSPVTETRTYHDVKEICKCDVDEFVILELGDFNDITETCSCSCSSSKSVTYEPDFNSAELLAKELYRVF
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<210> 13
<212> DNA
<213> Homo sapiens

<400> 13

13>Ly1462P, Old-SEQ-ID_6411, partial cDNA
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<210> 14
<212> DNA
<213> Homo sapiens

<400> 14

14>Ly1462P, Human Epstein-Barr virus complement receptor type II(cr2)_full-length
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<210> 15
<212> PRT
<213> Homo sapiens

<400> 15

15>Ly1462P, CR2/CD21/C3d/Epstein-Barr virus receptor, full-length
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<210> 16
<212> DNA
<213> Homo sapiens

<400> 16

16>Ly1484P, Old-SEQ-ID_10493, partial cDNA
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<210> 17
<212> DNA
<213> Homo sapiens

<400> 17

17>Ly1484P, KIAA1607, full-length cDNA
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<210> 18
<212> PRT
<213> Homo sapiens

<400> 18

18>Lyl484P, KIAA1607, full-length protein

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<210> 19
<212> DNA
<213> Homo sapiens

<400> 19

19>Ly1486P, Old-SEQ-ID_5058, partial cDNA
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ttccag

<210> 20
<212> DNA
<213> Homo sapiens

<400> 20

20>Ly1486P, Fc fragment of IgE, low affinity II, receptor for (CD23A), full-length
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<210> 21
<212> PRT
<213> Homo sapiens

<400> 21

21>Ly1486P, Fc fragment of IgE, low affinity II, receptor for (CD23A)_full-length
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<210> 22
<212> DNA
<213> Homo sapiens

<400> 22

22>Ly1677P, novel, partial, cDNA
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<210> 23
<212> DNA
<213> Homo sapiens

<400> 23

23>Ly1682P, novel, partial cDNA
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<210> 24
<212> DNA
<213> Homo sapiens

<400> 24

24>Ly1693P, Old-SEQ-ID_2611, partial cDNA
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<210> 25
<212> DNA
<213> Homo sapiens

<400> 25

25>Ly1693P, CXCR4, full-length cDNA
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<210> 26
<212> PRT
<213> Homo sapiens

<400> 26

26>Ly1693P, CXCR4, full-length protein
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<210> 27
<212> DNA
<213> Homo sapiens

<400> 27

27>Ly1697P, novel, partial cDNA
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<210> 28
<212> DNA
<213> Homo sapiens

<400> 28

28>Ly1715P, lectin-like NK cell receptor (LLT1), full-length cDNA
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<210> 29
<212> PRT
<213> Homo sapiens

<400> 29

29>Ly1715P, lectin-like NK cell receptor, full-length protein
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<210> 30
<212> DNA
<213> Homo sapiens

<400> 30

30>Ly1727P, Old-SEQ-ID_6042, partial cDNA
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tggctgccactactttgg

<210> 31
<212> DNA
<213> Homo sapiens

<400> 31

31>Ly1727P, pim-2 protooncogene homolog pim-2h, full-length cDNA
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<210> 32
<212> PRT
<213> Homo sapiens

<400> 32

32>Ly1727P, pim-2 proto-oncogene homolog pim-2h, full-length protein
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WSPLSDSVTCPLEVALLWKVGAGGGHPGVIRLLDWFETQEGFMLVLERPLPAQDLFDYITEKGPLGEGPS
RCFFGQVVAAIQHCHSRGVVHRDIKDENILIDLRRGCAKLIDFGSGALLHDEPYTDFDGTRVYSPPEWIS
RHQYHALPATVWSLGILLYDMVCGDIPFERDQEILEAELHFPAHVSPDCCALIRRCLAPKPSSRPSLEEI
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<210> 33
<212> DNA
<213> Homo sapiens

<400> 33

33>Ly1885P_DKFZp564F112 (from clone DKFZp564F112)_partial cDNA
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<210> 34
<212> DNA
<213> Homo sapiens

<400> 34

34>Ly1885P, CCP8 mRNA, full-length cDNA
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<210> 35
<212> DNA
<213> Homo sapiens

<400> 35

35>Ly1885P, CCP8, full-length protein
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TAYPALEETSSTIEAEEQKIPEDSIYIGTASDDSDIVTLEPPKLEEIGNQEVVIVEEAQSSEDFNMGSSS
SSQYTFCQPETVFSSQPSDDESSSDETSNQPSPAFRRRRARKKTVSASESEDRLVAEQETEPSKELSKRQ
FSSGLNKCVILALVIAISMGFGHFYGTIQIQKRQQLVRKIHEDELNDMKDYLSQCQQEQESFIDYKSLKE
NLARCWTLTEAEKMSFETQKTNLATENQYLRVSLEKEEKALSSLQEELNKLREQIRILEDKGTSTELVKE
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KKEIAILRERLTELERKLTFEQQRSDLWERLYVEAKDQNGKQGTDGKKKGGRGSHRAKNKSKETFLGSVK
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KPRTVFSDYLHPQYKAPTENHSRPYYAKRWKEEKPVHFKEFRKNTNSKKCSPGHDCRENSHSFRKACSGV
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<210> 36
<212> DNA
<213> Homo sapiens

<400> 36

36>Ly1905P_Old-SEQ-ID_546, partial cDNA
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tggctgccactactttgg

<210> 37
<212> PRT
<213> Homo sapiens

<400> 37

37>Ly1905P, Old-SEQ-ID_2169, partial protein
QVVAXIQHCHSRGVVHRDIKDENILIDLRRGCAKLIDFGSGALLHDEPYTDFDGTRVYSP
PEWISRHQYHALPATVWSLGIXLYDM

<210> 38
<212> DNA
<213> Homo sapiens

<400> 38

38>Ly1905P_Old_SEQ-ID_5277 partial cDNA
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<210> 39
<212> DNA
<213> Homo sapiens

<400> 39

39>Ly1905P pim-2 oncogene_ full-length cDNA
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<210> 40

<212> PRT
<213> Homo sapiens

<400> 40

40>Ly1905P pim-2 oncogene full-length
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WSPLSDSVTCPLEVALLWKVGAGGGHPGVIRLLDWFETQEGFMLVLERPLPAQDLFDYITEKGPLGEGPS
RCFFGQVVAAIQHCHSRGVVHRDIKDENILIDLRRGCAKLIDFGSGALLHDEPYTDFDGTRVYSPPEWIS
RHQYHALPATVWSLGILLYDMVCGDIPFERDQEILEAELHFPAHVSPDCCALIRRCLAPKPSSRPSLEEI
LLDPWMQTPAEDVPLNPSKGGPAPLAWSLLP

<210> 41
<212> DNA
<213> Homo sapiens

<400> 41

41>Ly663S_Old_SEQ-ID_2757 partial cDNA
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<210> 42
<212> DNA
<213> Homo sapiens

<400> 42

42>Ly663S CD37 antigen (CD37) full-length cDNA
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<210> 43
<212> PRT
<213> Homo sapiens

<400> 43

43>Ly663S, CD37 antigen, full-length
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IALLGCVGALKELRCLLGLYFGMLLLLFATQITLGILISTQRAQLERSLRDVVEKTIQKYGTNPEETAAE
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R

<210> 44
<212> DNA
<213> Homo sapiens

<400> 44

44>Ly664S, FLJ90810 fis, clone weakly similar to PROTEIN DISULFIDE ISOMERASE-
RELATED PROTEIN PRECURSOR, full-length

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<210> 45
<212> PRT
<213> Homo sapiens

<400> 45

45>Ly664S, full-length
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HRFVLSQAKDEL

<210> 46
<212> DNA
<213> Homo sapiens

<400> 46

46>Ly667S, Old-SEQ-ID_9413, partial cDNA
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tgtttcaacttcatccgtgtcctggtttcttacaatgtcacccatctctacacctgcggc
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accaccttcct

<210> 47
<212> DNA
<213> Homo sapiens

<400> 47

47>Ly667S, Semaphorin B, full-length
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cctgccaccaatacacacgcttctgctgcctggggctctcctattggtcctcgggggatgtggtaagaa
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<210> 48
<212> PRT
<213> Homo sapiens

<400> 48

48>Ly667S, Semaphorin B, full-length
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GDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLY
TCGTFAPSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHTAVLVDGMLYSGTMNNFLGSEPILMR
TLGSQPVLKTDNFLRWLHHDASFVAAIPSTQVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQ
KKWTTFLKAQLLSAPSRGSCPSTSSATRSCSPPILPQLPTSTQSSPPSGQVGGTRSSAVCAFSLLDIERV
FKGKFKELNKETSRWTTYRGPETNPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLA
VETAQGLDGHSHLVMYLGTTTGSLHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGAVFVGFSGGV
WRVPRANCSVYESCVDCVLARDPHCAWDPESRTCCLLSAPNLNSWKQDMERGNPEWACASGPMSRSLRPQ
SRPQIIKEVLAVPNSILELPCPHLSALASYYWSHGPAAVPEASSTVYNGSLLLIVQDGVGGLYQCWATEN
GFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWPHFVTVTVLFALVLSGAL
IILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA

<210> 49
<212> DNA
<213> Homo sapiens

<400> 49

49>Ly677S, Old-SEQ-ID_465, partial cDNA
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acatgggggagggcaccaagaaccgaatcatcacagccgaggggatcatcctcctgttct
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gg

<210> 50
<212> PRT
<213> Homo sapiens

<400> 50

50>Ly677S, Old-SEQ-ID_1923, partial protein
QQSCGTYLRVRQPPPRPFLDMGEGTKNRIITAEGIILLFCAVVPGTLLLXRKRWQERXLX

<210> 51
<212> DNA
<213> Homo sapiens

<400> 51

51>Ly677S, Old-SEQ-ID_5989, partial cDNA
accagcagtcctgcggcacctacctccgcgtgcgccagccgccccccaggcccttcctgg
acatgggggagggcaccaagaaccgaatcatcacagccgaggggatcatcctcctgttct
gcgcggtggtgcctgggacgctgctgctgttnaggaaacgatggcaagaacganaactcn
gg

<210> 52
<212> PRT
<213> Homo sapiens

<400> 52

52>Ly677S, Old-SEQ-ID_1496, partial protein
QQSCGTYLRVRQPPPRPFLDMGEGTKNRIITAEGIILLFCAVVPGTLLLXRKRWQERXLX

<210> 53
<212> DNA
<213> Homo sapiens

<400> 53

53>Ly677S, CD79A antigen (immunoglobulin-associated alpha), full-length
tgctgcaactcaaactaaccaacccactgggagaagatgcctgggggtccaggagtcctccaagctctgc
ctgccaccatcttcctcctcttcctgctgtctgctgtctacctgggccctgggtgccaggccctgtggat
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<210> 54
<212> PRT
<213> Homo sapiens

<400> 54

54>Ly677S, CD79A antigen, complete protein
MPGGPGVLQALPATIFLLFLLSAVYLGPGCQALWMHKVPASLMVSLGEDAHFQCPHNSSNNANVTWWRVL
HGNYTWPPEFLGPGEDPNGTLIIQNVNKSHGGIYVCRVQEGNESYQQSCGTYLRVRQPPPRPFLDMGEGT
KNRIITAEGIILLFCAVVPGTLLLFRKRWQNEKLGLDAGDEYEDENLYEGLNLDDCSMYEDISRGLQGTY
QDVGSLNIGDVQLEKP

<210> 55
<212> DNA
<213> Homo sapiens

<400> 55

55>Ly1891P, orphan G-protein coupled receptor (GPRC5D), full-length
atgtacaaggactgcatcgagtccactggagactattttcttctctgtgacgccgaggggccatggggca
tcattctggagtccctggccatacttggcatcgtggtcacaattctgctactcttagcatttctcttcct
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<210> 56
<212> PRT
<213> Homo sapiens

<400> 56

56>Ly1891P, orphan G-protein coupled receptor (GPRC5D), full-length
MYKDCIESTGDYFLLCDAEGPWGIILESLAILGIVVTILLLLAFLFLMRKIQDCSQWNVLPTQLLFLLSV
LGLFGLAFAFIIELNQQTAPVRYFLFGVLFALCFSCLLAHASNLVKLVRGCVSFSWTTILCIAIGCSLLQ
IIIATEYVTLIMTRGMMFVNMTPCQLNVDFVVLLVYVLFLMALTFFVSKATFCGPCENWKQHGRLIFITV
LFSIIIWVVWISMLLRGNPQFQRQPQWDDPVVCIALVTNAWVFLLLYIVPELCILYRSCRQECPLQGNAC
PVTAYQHSFQVENQELSRARDSDGAEEDVALTSYGTPIQPQTVDPTQECFIPQAKLSPQQDAGGV

<210> 57
<212> DNA
<213> Homo sapiens

<400> 57

57>CD138,syndecan 1 (SDC1), full-length cDNA
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ccgagcggagaggaatccggcagtagagagcggactccagccggcggaccctgcagccctcgcctgggac
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taaagta

<210> 58
<212> PRT
<213> Homo sapiens

<400> 58

58>CD138,syndecan 1 (SDC1), full-length protein
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LTAIPTSPEPTGLEATAASTSTLPAGEGPKEGEAVVLPEVEPGLTAREQEATPRPRETTQLPTTHQASTT
TATTAQEPATSHPHRDMQPGHHETSTPAGPSQADLHTPHTEDGGPSATERAAEDGASSQLPAAEGSGEQD
FTFETSGENTAVVAVEPDRRNQSPVDQGATGASQGLLDRKEVLGGVIAVGLVGLIFAVCLVGFMLYRMKK
KDEGSYSLEEPKQANGGAYQKPTKQEEFYA

<210> 59
<212> DNA
<213> Homo sapiens

<400> 59

59>CD22, Old-SEQ-ID_4021, partial cDNA
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tctgaagggccttttccacctcatatccagctccctccagaaattcaagagtcccaggaa
gtcactctgacctgcttgctgaatttctcctgctatgggtatccgatccaattgcagtgg
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gtgacctgccagcttcaggatgcagatgggaagttcctctccaatgacacggtgcag

<210> 60
<212> DNA
<213> Homo sapiens

<400> 60

60>CD22, full-length cDNA
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<210> 61
<212> PRT
<213> Homo sapiens

<400> 61

61>CD22, full-length protein
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FPPHIQLPPEIQESQEVTLTCLLNFSCYGYPIQLQWLLEGVPMRQAAVTSTSLTIKSVFTRSELKFSPQW
SHHGKIVTCQLQDADGKFLSNDTVQLNVKHTPKLEIKVTPSDAIVREGDSVTMTCEVSSSNPEYTTVSWL
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FLCMSLANPLPTNYTWYHNGKEMQGRTEEKVHIPKILPWHAGTYSCVAENILGTGQRGPGAELDVQYPPK
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CSWASPVALNVQYAPRDVRVRKIKPLSEIHSGNSVSLQCDFSSSHPKEVQFFWEKNGRLLGKESQLNFDS
ISPEDAGSYSCWVNNSIGQTASKAWTLEVLYAPRRLRVSMSPGDQVMEGKSATLTCESDANPPVSHYTWF
DWNNQSLPHHSQKLRLEPVKVQHSGAYWCQGTNSVGKGRSPLSTLTVYYSPETIGRRVAVGLGSCLAILI
LAICGLKLQRRWKRTQSQQGLQENSSGQSFFVRNKKVRRAPLSEGPHSLGCYNPMMEDGISYTTLRFPEM

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DYVILKH

<210> 62
<212> DNA
<213> Homo sapiens

<400> 62

62>CD79beta, old-SEQ-ID_504, partial cDNA
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gccagggagcctgcacccaggtcatggggcgacctggctctcactcctggcctgggtgct
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<210> 63
<212> PRT
<213> Homo sapiens

<400> 63

63>CD79beta, old-SEQ-ID_1747, partial protein
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VTLRTGEVKWSVGEHPGQE

<210> 64
<212> DNA
<213> Homo sapiens

<400> 64

64>CD79beta, Old-SEQ-ID_5238, partial cDNA
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<210> 65
<212> DNA
<213> Homo sapiens

<400> 65

65>CD79beta, full-length cDNA
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<210> 66

<212> PRT
<213> Homo sapiens

<400> 66

66>CD79beta, full-length protein
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SGNVSWLWKQEMDENPQQLKLEKGRMEESQNESLATLTIQGIRFEDNGIYFCQQKCNNTSEVYQGCGTEL
RVMGFSTLAQLKQRNTLKDGIIMIQTLLIILFIIVPIFLLLDKDDSKAGMEEDHTYEGLDIDQTATYEDI
VTLRTGEVKWSVGEHPGQE

<210> 67
<212> DNA
<213> Homo sapiens

<400> 67

67>Ly1450P, Old-SEQ-ID_6695, partial cDNA
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cctctcaagtgttgcattgtccctgcctaaaccaagaaggctaaacaaagcccctcctgt
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<210> 68
<212> DNA
<213> Homo sapiens

<400> 68

68>Ly1450P, partial cDNA
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<210> 69
<212> DNA
<213> Homo sapiens

<400> 69

69>Ly1451P, Old-SEQ-ID_3507, partial cDNA
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<210> 70
<212> DNA
<213> Homo sapiens

<400> 70

70>Ly1451P, partial cDNA
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gctacataccttggatagat

71>Ly1451P, partial protein
MDSRGSPLGGLGLPCGASLRRTPASPSDAIQRALPGRKLPRWNASPEQRVAVPCGGLTQWLNTGKELALGVRTSETCRLG
AVHGWEQLHQPLQSDSEEDDKPCSSHTRKLTGPRTAEA

72>Ly1454P, Old-SEQ-ID_3577, partial cDNA
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ccagaagcaaagacaaagattgcatgttgttcttacagatgacttaaatcatctctttga
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73>Ly1454P, FLJ40597, full-length cDNA
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tgttgtagtcagtaactgtttctatttccaggcatttttagatgaattcactaactggtcaagaataaat
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74>Ly1454P, FLJ40597, full-length protein
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RSPKLFVVFFDNQAYPEYLITFTA

75>Ly1485P, Old-SEQ-ID_2789, partial cDNA
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76>Ly1485P, Old-SEQ-ID_2417, partial protein
RSHLTLLYCSAVKSASFTGGKGPQSLRRASLETGWFFLCSPESPSDEKGGLETECQKPIK
GTALHFREGAGLEKNQRSS

77>Ly1485P, Old-SEQ-ID_10476, partial cDNA
ggcacgagcaatgggacttatcgctgctgatgttaaccttgatctcttggttcaggtggt
gcctgccagctgtctccactgtggagttactatttttccttttccccattttattcatca
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78>Ly1500P, Old-SEQ-ID_5226, partial cDNA
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79>Ly1500P, splice-1, FLJ20706, complete cDNA
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80>Ly1500P, splice-1 FLJ20706, full-length protein
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81>Ly1500P, splice-2 DKFZp667N1611, full-length cDNA
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82>Ly1500P, splice-2, DKFZp667N1611, full-length protein
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83>Ly1500P, splice-3, FLJ34204 fis, full-length cDNA
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84>Ly1500P, splice-3, FLJ34204 fis, full-length protein
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SNSLLRDLTPKKCQFLEKILHSPKSVVTLLCGVKSSDQLYELLNISQSRWEISTEQEPEDYISVIQSIIF
KDSEDYFEVNIPTDLRAKHSGEISERKEIEELSEASRNTIPLAVVLPTEIPCEDPGEIFIILRDEVIGDT
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GESLCQNSIEELDGVLTSIFKHEIPYYEFQSLQTEICSQNKYTHFKELPTLLHCAAKFGLKNLAIHLLQC
SGATWASKMKNMEGSDPTHIAERHGHKELKKIFEDFSIQEIDINNEQENDYEEDIASFSTYIPSTQNPAF
HHESRKTYGQSADGAEANEMEGEGKQNGSGMETKHSPLEVGSESSEDQYDDLYVFIPGADPENNSQEPLM
SSRPPLPPPRPVANAFQLERPHFTLPGTMVEGQMERSQNWGHPGVRQETGDEPKGEKEKKEEEKEQEEEE
DPYTFAEIDDSEYDMILANLSIKKKTGSRSFIINRPPAPTPRPTSIPPKEETTPYIAQVFQQKTARRQSD
DDKFRGLPKKQDRARIESPAFSTLRGCLTDGQEELILLQEKVKNGKMSMDEALEKFKHWQMGKSGLEMIQ
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85>Ly1516P, Old-SEQ-ID_8949, partial cDNA
cctctcagaaaactgagcatactagcaagacagctcttcttgaaaaaaaaaatatgtata
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86>Ly1516P, Similar to CD47 antigen, splice_form-1,full-length cDNA
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87>Ly1516P, Similar to CD47 antigen, splice_form-1, full-length protein
MWPLVAALLLGSACCGSAQLLFNKTKSVEFTFCNDTVVIPCFVTNMEAQNTTEVYVKWKFKGRDIYTFDG
ALNKSTVPTDFSSAKIEVSQLLKGDASLKMDKSDAVSHTGNYTCEVTELTREGETIIELKYRVVSWFSPN
ENILIVIFPIFAILLFWGQFGIKTLKYRSGGMDEKTIALLVAGLVITVIVIVGAILFVPGEYSLKNATGL
GLIVTSTGILILLHYYVFSTAIGLTSFVIAILVIQVIAYILAVVGLSLCIAACIPMHGPLLISGLSILAL
AQLLGLVYMKFVASNQKTIQPPRNN

88>Ly1516P, cDNA DKFZp313F0317, splice_form-2, partial cDNA
ggagatattttcttgttcaatttaaggagaggtaaatttggtatcaatagaaaaaatgtttctgaaaaat
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98>Ly1712P, partial cDNA
ccacaaaataaggtctaattcaataaattatagtaaattaatgtaatataatattacatgccactaaaaagaataaggta
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99>Ly1729P, Old-SEQ-ID_6586, partial cDNA

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gaaaatctcctcagagg

100>Ly1729P, hematopoietic cell-specific Lyn substrate 1 (HCLS1), full-length cDNA
aattccgccgggcgcttagaacagaggcttgcacaggtggagatgtggaagtctgtagtgggccatgatg
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101>Ly1729P, hematopoietic cell-specific Lyn substrate 1 (HCLS1), full-length protein
MWKSVVGHDVSVSVETQGDDWDTDPDFVNDISEKEQRWGAKTIEGSGRTEHINIHQLRNKVSEEHDVLRK
KEMESGPKASHGYGGRFGVERDRMDKSAVGHEYVAEVEKHSSQTDAAKGFGGKYGVERDRADKSAVGFDY
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102>Ly1848P, partial cDNA
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gagtttagcaaggatg

103>Ly1859P, old-SEQ-ID_640, partial cDNA
ccagagtgcaggatacatcattggcaccaagggtctttttcaattcttggtcaatcctct
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104>Ly1859P, old-SEQ-ID_2452, partial protein
LADQCLTTALNCDQAAQRLERVRGRVLKKFKSDSGLAQRRFIRGWGLCIFLPFVLSQLEP
GCKKELPEFEGDVLAVGSQALTTEGIYEDVIRGCLLQRIDQELKKTLGANDVSCTL

105>Ly1859P, Old-SEQ-ID_3313, partial cDNA
ctgcaagacagcagagaanctgccaatatccagttagcagatgactttgctggcaagcag
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106>Ly1859P, FLJ00140, full-length cDNA
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107>Ly1859P, FLJ00140, full-length protein
QAVVVGKGRGAPGDDSSMGGRPSSPLDKQQRQHLRGQVDTLLRNFLPCYRGQLAASVLRQISRELGPQEP
TGSQLLRSKKLPRVREHRGPLTQLRGHPPRWQPIFCVLRGDGRLEWFSHKEEYENGGHCLGSTALTGYTL
LTSQREYLRLLDALCPESLGDHTQEEPDSLLEVPVSFPLFLQHPFRRHLCFSAATREAQHAWRLALQGGI
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FKRSSHLGLPSSWDYRHPL

108>Ly1866P, Similar to hypothetical protein PRO1722, full-length cDNA
ctagaatgctaattgcacttaggcctcatggttctagtaaacggcagctgtgggccctttttgcctcttcc
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109>Ly1866P, Similar to hypothetical protein PRO1722, full-length protein
MESRSVAQAGVQWPDLGSLQPLPPRFKRFFCLSLQSSWDYRHAPPRPANFVFLVETGFCHVSQAGLELLT
SSDPPPRPPKVLR

110>Ly1867P, Old-SEQ-ID_3570, partial cDNA
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111>Ly1868P, partial cDNA
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113>Ly669S, intercellular adhesion molecule 3 (ICAM3), complete cDNA
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114>Ly669S, intercellular adhesion molecule 3, complete protein
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115>Ly672S, Old-SEQ-ID_3042, partial cDNA
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116>Ly672S, cisplatin resistance related protein CRR9p, full-length cDNA
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117>Ly672S, cisplatin resistance related protein CRR9p, full-length protein
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118>Ly675S, KIAA0906 gene, partial cDNA
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119>Ly675S, KIAA0906 protein, partial protein
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<213> Homo sapiens

<400> 121
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20 25 30
Gln Pro Ser Ala Glu Ala Ala Ala Ala Pro Ser Leu Ala Asn Ile Ser
35 40 45

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Cys Phe Thr Gln Lys Leu Val Glu Lys Leu Tyr Ser Gly Met Phe Ser
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Ala Asp Pro Arg His Ile Leu Leu Phe Ile Leu Glu His Ile Met Val
65                  70                  75                  80
Val Ile Glu Thr Ala Ser Ser Gln Arg Asp Thr Val Leu Ser Thr Leu
                85                  90                  95
Tyr Ser Ser Leu Asn Lys Val Ile Leu Tyr Cys Leu Ser Lys Pro Gln
            100                 105                 110
Gln Ser Leu Ser Glu Cys Leu Gly Leu Leu Ser Ile Leu Gly Phe Leu
        115                 120                 125
Gln Glu His Trp Asp Val Val Phe Ala Thr Tyr Asn Ser Asn Ile Ser
    130                 135                 140
Phe Leu Leu Cys Leu Met His Cys Leu Leu Leu Leu Asn Glu Arg Ser
145                 150                 155                 160
Tyr Pro Glu Gly Phe Gly Leu Glu Pro Lys Pro Arg Met Ser Thr Tyr
                165                 170                 175
His Gln Val Phe Leu Ser Pro Asn Glu Asp Val Lys Glu Lys Arg Glu
            180                 185                 190
Asp Leu Pro Ser Leu Ser Asp Val Gln His Asn Ile Gln Lys Thr Val
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Gln Thr Leu Trp Gln Gln Leu Val Ala Gln Arg Gln Gln Thr Leu Glu
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Asp Ala Phe Lys Ile Asp Leu Ser Val Lys Pro Gly Glu Arg Glu Val
225                 230                 235                 240
Lys Ile Glu Glu Val Thr Pro Leu Trp Glu Glu Thr Met Leu Lys Ala
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Trp Gln His Tyr Leu Ala Ser Glu Lys Lys Ser Leu Ala Ser Arg Ser
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Asn Val Ala His His Ser Lys Val Thr Leu Trp Ser Gly Ser Leu Ser
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Lys Thr Glu Asp Phe Val Ser Cys Ile Glu Asn Tyr Arg Arg Arg Gly
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Gln Glu Leu Tyr Ala Ser Leu Tyr Lys Asp His Val Gln Arg Arg Lys
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Cys Gly Asn Ile Lys Ala Ala Asn Ala Trp Ala Arg Ile Gln Glu Gln
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Cys Ser Pro Trp Glu Leu Asp Trp Arg Glu Gly Pro Ala Arg Met Arg
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His Lys Glu Ser Gln Asp Lys Asn Asp His Ile Ser Gln Thr Asn Ala
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Glu Val Gly Val Asp Cys Thr Gln Leu Thr Phe Phe Pro Ala Leu His
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Glu Ser Leu His Ser Glu Asp Phe Leu Glu Leu Cys Arg Glu Arg Gln
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Val Ile Leu Gln Glu Leu Leu Asp Lys Glu Lys Val Thr Gln Lys Phe
465                 470                 475                 480
Ser Leu Val Ile Val Gln Gly His Leu Val Ser Glu Gly Val Leu Leu
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Phe Gly His Gln His Phe Tyr Ile Cys Glu Asn Phe Thr Leu Ser Pro
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Arg Phe Leu Leu Gln Asp Ile Ala Leu Glu Ile Phe Phe His Asn Gly
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625                 630                 635                 640
Tyr Leu Asn Thr Ala Ala Gly Arg Thr Cys Asn Asp Tyr Met Gln Tyr
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Pro Val Phe Pro Trp Val Leu Ala Asp Tyr Thr Ser Glu Thr Leu Asn
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Leu Ala Asn Pro Lys Ile Phe Arg Asp Leu Ser Lys Pro Met Gly Ala
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Asp Pro Arg Lys Phe Ile Ser Leu His Arg Lys Ala Leu Glu Ser Asp
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Lys Gln Gln Gly Pro Ala Ala Val Asp Ala Val Asn Ile Phe His Pro
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Lys Val Leu Met Thr Phe Glu Asn Leu Ala Ala Trp Gly Arg Cys Leu
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Cys Ala Val Cys Pro Ser Pro Thr Thr Ile Val Thr Ser Gly Thr Ser
1025                1030                1035                1040
Thr Val Val Cys Val Trp Glu Leu Ser Met Thr Lys Gly Arg Pro Arg
                1045                1050                1055
Gly Leu Arg Leu Arg Gln Ala Leu Tyr Gly His Thr Gln Ala Val Thr
            1060                1065                1070
Cys Leu Ala Ala Ser Val Thr Phe Ser Leu Leu Val Ser Gly Ser Gln
        1075                1080                1085
Asp Cys Thr Cys Ile Leu Trp Asp Leu Asp His Leu Thr His Val Thr
    1090                1095                1100
Arg Leu Pro Ala His Arg Glu Gly Ile Ser Ala Ile Thr Ile Ser Asp
1105                1110                1115                1120
Val Ser Gly Thr Ile Val Ser Cys Ala Gly Ala His Leu Ser Leu Trp
                1125                1130                1135
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Asn Val Asn Gly Gln Pro Leu Ala Ser Ile Thr Thr Ala Trp Gly Pro
            1140                1145                1150
Glu Gly Ala Ile Thr Cys Cys Cys Leu Met Glu Gly Pro Ala Trp Asp
        1155                1160                1165
Thr Ser Gln Ile Ile Ile Thr Gly Ser Gln Asp Gly Met Val Arg Val
    1170                1175                1180
Trp Lys Thr Glu Asp Val Lys Met Ser Val Pro Gly Arg Pro Ala Gly
1185                1190                1195                1200

Glu Glu Pro Leu Ala Gln Pro Pro Ser Pro Arg Gly His Lys Trp Glu
                1205                1210                1215
Lys Asn Leu Ala Leu Ser Arg Glu Leu Asp Val Ser Ile Ala Leu Thr
            1220                1225                1230
Gly Lys Pro Ser Lys Thr Ser Pro Ala Val Thr Ala Leu Ala Val Ser
        1235                1240                1245
Arg Asn His Thr Lys Leu Leu Val Gly Asp Glu Arg Gly Arg Ile Phe
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Cys Trp Ser Ala Asp Gly
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            20                  25                  30
Tyr Pro Val Phe Pro Trp Val Leu Ala Asp Tyr Thr Ser Glu Thr Leu
        35                  40                  45
Asn Leu Ala Asn Pro Lys Ile Phe Arg Asp Leu Ser Lys Pro Met Gly
    50                  55                  60
Ala Gln Thr Lys Glu Arg Lys Leu Lys Phe Ile Gln Arg Phe Lys Glu
65                  70                  75                  80
Val Glu Lys Thr Glu Gly Asp Met Thr Val Gln Cys His Tyr Tyr Thr
                85                  90                  95
His Tyr Ser Ser Ala Ile Ile Val Ala Ser Tyr Leu Val Arg Met Pro
            100                 105                 110
Pro Phe Thr Gln Ala Phe Cys Ala Leu Gln Gly Gly Ser Phe Asp Val
        115                 120                 125
Ala Asp Arg Met Phe His Ser Val Lys Ser Thr Trp Glu Ser Ala Ser
    130                 135                 140
Arg Glu Asn Met Ser Asp Val Arg Glu Leu Thr Pro Glu Phe Phe Tyr
145                 150                 155                 160
Leu Pro Glu Phe Leu Thr Asn Cys Asn Gly Val Glu Phe Gly Cys Met
                165                 170                 175
Gln Asp Gly Thr Val Leu Gly Asp Val Gln Leu Pro Pro Trp Ala Asp
            180                 185                 190
Gly Asp Pro Arg Lys Phe Ile Ser Leu His Arg Lys Ala Leu Glu Ser
        195                 200                 205
Asp Phe Val Ser Ala Asn Leu His His Trp Ile Asp Leu Ile Phe Gly
    210                 215                 220
Tyr Lys Gln Gln Gly Pro Ala Ala Val Asp Ala Val Asn Ile Phe His
225                 230                 235                 240
Pro Tyr Phe Tyr Gly Asp Arg Met Asp Leu Ser Ser Ile Thr Asp Pro
                245                 250                 255
Leu Ile Lys Ser Thr Ile Leu Gly Phe Val Ser Asn Phe Gly Gln Val
            260                 265                 270
Pro Lys Gln Leu Phe Thr Lys Pro His Pro Ala Arg Thr Ala Ala Gly
        275                 280                 285
Lys Pro Leu Pro Gly Lys Asp Val Ser Thr Pro Val Ser Leu Pro Gly
    290                 295                 300
His Pro Gln Pro Phe Phe Tyr Ser Leu Gln Ser Leu Arg Pro Ser Gln
305                 310                 315                 320
Val Thr Val Lys Asp Met Tyr Leu Phe Ser Leu Gly Ser Glu Ser Pro
                325                 330                 335
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Lys Gly Ala Ile Gly His Ile Val Ser Thr Glu Lys Thr Ile Leu Ala
            340                 345                 350
Val Glu Arg Asn Lys Val Leu Leu Pro Pro Leu Trp Asn Arg Thr Phe
        355                 360                 365
Ser Trp Gly Phe Asp Asp Phe Ser Cys Cys Leu Gly Ser Tyr Gly Ser
    370                 375                 380
Asp Lys Val Leu Met Thr Phe Glu Asn Leu Ala Ala Trp Gly Arg Cys
385                 390                 395                 400
Leu Cys Ala Val Cys Pro Ser Pro Thr Thr Ile Val Thr Ser Gly Thr
                405                 410                 415
Ser Thr Val Val Cys Val Trp Glu Leu Ser Met Thr Lys Gly Arg Pro
            420                 425                 430
Arg Gly Leu Arg Leu Arg Gln Ala Leu Tyr Gly His Thr Gln Ala Val
        435                 440                 445
Thr Cys Leu Ala Ala Ser Val Thr Phe Ser Leu Leu Val Ser Gly Ser
    450                 455                 460
Gln Asp Cys Thr Cys Ile Leu Trp Asp Leu Asp His Leu Thr His Val
465                 470                 475                 480
Thr Arg Leu Pro Ala His Arg Glu Gly Ile Ser Ala Ile Thr Ile Ser
                485                 490                 495
Asp Val Ser Gly Thr Ile Val Ser Cys Ala Gly Ala His Leu Ser Leu
            500                 505                 510
Trp Asn Val Asn Gly Gln Pro Leu Ala Ser Ile Thr Thr Ala Trp Gly
        515                 520                 525
Pro Glu Gly Ala Ile Thr Cys Cys Cys Leu Met Glu Gly Pro Ala Trp
    530                 535                 540
Asp Thr Ser Gln Ile Ile Ile Thr Gly Ser Gln Asp Gly Met Val Arg
545                 550                 555                 560
Val Trp Lys Thr Glu Asp Val Lys Met Ser Val Pro Gly Arg Pro Ala
                565                 570                 575
Gly Glu Glu Pro Leu Ala Gln Pro Pro Ser Pro Arg Gly His Lys Trp
            580                 585                 590
Glu Lys Asn Leu Ala Leu Ser Arg Glu Leu Asp Val Ser Ile Ala Leu
        595                 600                 605
Thr Gly Lys Pro Ser Lys Thr Ser Pro Ala Val Thr Ala Leu Ala Val
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<210> 124
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<212> DNA
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human endogenous retroviral sequence (HERV)

<400> 124

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